

GenCore version 4.5
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Om nucleic - nucleic search, using sw model
Run on: December 27, 2001, 16:53:25 ; Search time 4492.43 Seconds
(without alignments) 6649.689 Million cell updates/sec

Title: US-09-830-647-3

Perfect score: 2780

Sequence: 1 aattcgagacgactcttg.....aaaaaaaactcggag 2780

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:*

1: em_estfun:*

2: em_esthum:*

3: em_estin:*

4: em_estom:*

5: em_estpli:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_estti:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_fun:*

14: em_gss_hum:*

15: em_gss_inv:*

16: em_gss_pln:*

17: em_gss_pro:*

18: em_gss_rnd:*

19: em_gss_vrt:*

20: em_gss_other:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1	REFID	AL560180	LOCUS	AL560180	950 bp	mRNA	DEFINITION	AL560180	EST	16-FEB-2001	PRIMER
ACCESSION				VERSION	AL560180.1	GI:12906394		KEYWORDS	EST.			
SOURCE				ORGANISM	Homo sapiens							
REFERENCE				EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				AUTHORS	L.J.W.B., Gruber,C., Jesse,J. and Polayes,D.			
TITLE				VERSION	1 (bases 1 to 950)			JOURNAL	Full-length cDNA libraries and normalization			
COMMENT				KEYWORDS	Unpublished (2001)			CONTACT	Contact: Genoscope			
				ORGANISM	Genoscope - Centre National de Séquençage			EMAIL	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
FEATURES				SOURCE				LOCATION/QUALIFIERS	1. .950			
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									/db_xref="taxon:9606"			
									/clone="CS00C002YF20"			
									/clone_libr="LTI_FLO11_BCI"			
									/sex="male"			
									/tissue_type="B" cells from Burkitt lymphoma"			
									/lab_host="DRII0B"			
									/note="vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligonucleotide primer. Five prime end enriched double stranded cDNA was digested with Not I and cloned into the Not I and Eco RI sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Life Technologies, a division of Invitrogen"			

Result No.	Score	Query Match Length	DB ID	Description
1	949.2	34.1	950	10 AL560180
c	817.4	29.4	10 AL581669	AL581669 AL581669
c	769	27.7	10 AL548911	AL548911 AL548911
c	768.2	27.6	10 AL573294	AL573294 AL573294
c	756	27.2	10 AL572094	AL572094 602692613
c	723.4	26.0	10 AL559244	AL559244 AL559244
c	721.6	26.0	10 AL528881	AL528881 AL528881
c	719	25.9	10 AL580899	AL580899 AL580899
c	713.4	25.7	12 AK014480	AK014480 AK014480
c	712	25.6	11 BFR93466	MUS muscu
c	710	25.5	11 BG496289	BG496289 BG496289
c	710	10	10 AI948485	AI948485 AI948485

BASE COUNT	RESULT	2	EST	16-FEB-2001
ORIGIN	DEFINITION	AI581669	845 bp	mRNA
Query Match	34.1%	Score 94.9%; DB 10; Length 950;		
Best Local Similarity	99.8%	Pred. No. 3; Je-144; Mismatches 2; Indels 0; Gaps 0;		
Matches	948	Conservative		
Qy	311	cttgcggcttcctccggccgtggagccatcgcccccggaaacccggactcgca	370	
	1	CTTGCCTTCCTCCGGCCGTGGAGCCATCGCCCCCAGAACCCGACCTCGCA	60	
Db	371	gacggggatccccatctcgatggggccatctgggggggggggggggggggggggg	430	
	1	GACGGGGATCCTACACGGAGGCCCTAGTGGGGAGGGAGAGGGGGGGGGGG	120	
Db	61	gacggggatccccatctcgatggggccatctgggggggggggggggggggggggg	430	
	1	GACGGGGATCCTACACGGAGGCCCTAGTGGGGAGGGAGAGGGGGGGGGGG	120	
Qy	431	gtccacacggccggggaaaggcggtttgggggggggggggggggggggggggg	490	
	1	GTCACACGGCCGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	180	
Db	121	ccatcgatgg	550	
	1	CCATCGATGG	240	
Db	181	ccatcgatgg	550	
	1	CCATCGATGG	240	
Qy	551	ggacattccagggtggaaatccaaatggaaaaaacagaccatccggaaatct	610	
	1	GGACATTCCAGGGTGGATCAAGTCATAAATGAAAGAGACATCTGAACCT	300	
Db	241	tt	670	
	1	TT	670	
Qy	611	ctgaaacatcgatccatcgccggaaatccaaatcgatggccctttggggaaatgtt	360	
	1	CTGAAACATCGATACAGGGAAATCCAAATGTAAGGCCACTTGGGGAAATGTT	360	
Db	301	tatcttgacttctgttacccatatcgaaaactccaaagacattaaatgtatcg	730	
	1	TATCTTGACTTCTGTTCACCATATCGAAAACCTCAAGGACATTAAGCTG	420	
Qy	671	tt	730	
	1	TT	730	
Db	361	TACCTTGACTTCTGTTCACCATATCGAAAACCTCAAGGACATTAAGCTG	420	
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Qy	731	ggaggcggttt	790	
	1	GGAGGCGGTTT	790	
Db	421	ggaggcggttt	480	
	1	GGAGGCGGTTT	480	
Qy	791	gaagtcataatggacaaccttgggtggatctcgatccaaatggaaatctgtca	850	
	1	GAAGTCATAATGGACAACCTTGGGTGGATCTCGATCCAAATGGAAATCTGTCA	510	
Db	481	tt	510	
	1	TT	510	
Qy	851	tatactcgatccatcgatccatccatcgatggatccatcgatggatccatcgat	910	
	1	TATACCGATCCATCGATCCATCGATGGATCCATCGATGGATCCATCGAT	600	
Db	541	tt	600	
	1	TT	600	
Qy	911	gacacgtgtgtttttaatgggggggggggggggggggggggggggggggggggg	970	
	1	GACACGTGTGTGTAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	650	
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	1	TT	650	
Qy	971	tttatt	1030	
	1	TTTATT	1030	
Db	661	tt	720	
	1	TT	720	
Qy	1031	atgtatcgatccatcgatccatcgatccatcgatccatcgatccatcgatccat	1090	
	1	ATGTATCGATCCATCGATCCATCGATCCATCGATCCATCGATCCATCGATCC	780	
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Qy	1091	tt	1150	
	1	TT	1150	
Db	781	TTTATCGATCCATCGATCCATCGATCCATCGATCCATCGATCCATCGATCC	840	
	1	TTTATCGATCCATCGATCCATCGATCCATCGATCCATCGATCCATCGATCC	840	
Qy	1151	tt	1210	
	1	TT	1210	
Db	841	tt	900	
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Qy	1211	tt	1260	
	1	TT	1260	

		http://fulllength.invitrogen.com"
BASE COUNT	249	a 168 c 170 g 182 t
ORIGIN		
Query Match	27.7%	Score 769; DB 10; Length 769;
Matches	769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DEFINITION	AL573294 LTL_NFL006_PL2 Homo sapiens CDNA clone CS001043Y010 3	
ACCESSION	AL573294	
VERSION	AL573294.1	GI:12932397
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 769)	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished (2001)	
CONTACT	Genoscope - Centre National de Sequencing	
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1. .769	/db_xref="taxon:6606"	
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RESULT	4	
LOCUS	AL573294	AL573294 784 bp mRNA EST 16-FEB-2001
DEFINITION	AL573294 LTL_NFL006_PL2 Homo sapiens CDNA clone CS001043Y010 3	
ACCESSION	AL573294	
VERSION	AL573294.1	GI:12932397
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

Page
7

/tissue-type="T cells from T cell leukemia"
 /note="Vector: pcMSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pcMSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com>"

AK014480
 LOCUS AK014480 2338 bp mRNA HRC
 DEFINITION Mus musculus 14 days embryo liver cDNA, RIKEN full-length enriched
 library, clone:4432409B02, full insert sequence.
ACCESSION AK014480
VERSION AK014480_1 GI:15852363
KEYWORDS CAP trapper.
SOURCE Mus musculus (strain:c57BL/6J) 14 days embryo liver cDNA to mRNA,
 clone_4432409B02.
ORGANISM Mus musculus
 Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.

Fri Dec 28 08:22:46 2001

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